

E. Slobodsky

5

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/415,540

DATE: 11/09/1999
TIME: 15:46:25

INPUT SET: S33887.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

1
2
3 (1) General Information
4
5 (i) APPLICANT: Hawkins, Phillip R.
6 Hillman, Jennifer L.
7
8 (ii) TITLE OF THE INVENTION: A NOVEL HUMAN PYROPHOSPHATASE
9
10 (iii) NUMBER OF SEQUENCES: 5
11
12 (iv) CORRESPONDENCE ADDRESS:
13 (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
14 (B) STREET: 3174 Porter Drive
15 (C) CITY: Palo Alto
16 (D) STATE: California
17 (E) COUNTRY: USA
18 (F) ZIP: 94304
19
20 (v) COMPUTER READABLE FORM:
21 (A) MEDIUM TYPE: Diskette
22 (B) COMPUTER: IBM Compatible
23 (C) OPERATING SYSTEM: DOS
24 (D) SOFTWARE: FastSEQ Version 1.5
25
26 (vi) CURRENT APPLICATION DATA:
27 (A) APPLICATION NUMBER: 09/415,540
28 (B) FILING DATE:
29
30 (vii) PRIOR APPLICATION DATA:
31 (A) APPLICATION NUMBER: 08/741,437
32 (B) FILING DATE:
33
34 (viii) ATTORNEY/AGENT INFORMATION:
35 (A) NAME: Billings, Lucy J.
36 (B) REGISTRATION NUMBER: 36,749
37 (C) REFERENCE/DOCKET NUMBER: PF-0148 US
38
39 (ix) TELECOMMUNICATION INFORMATION:
40 (A) TELEPHONE: (415) 855-0555
41 (B) TELEFAX: (415) 845-4166
42
43
44 (2) INFORMATION FOR SEQ ID NO:1:
45
46 (i) SEQUENCE CHARACTERISTICS:

ENTERED

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47 (A) LENGTH: 289 amino acids
48 (B) TYPE: amino acid
49 (C) STRANDEDNESS: single
50 (D) TOPOLOGY: linear
51
52 (ii) MOLECULE TYPE: peptide
53
54 (vii) IMMEDIATE SOURCE:
55 (A) LIBRARY:
56 (B) CLONE: Consensus
57
58 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
59
60 Met Ser Gly Phe Ser Thr Glu Glu Arg Ala Ala Pro Phe Ser Leu Glu
61 1 5 10 15
62 Tyr Arg Val Phe Leu Lys Asn Glu Lys Gly Gln Tyr Ile Ser Pro Phe
63 20 25 30
64 His Asp Ile Pro Ile Tyr Ala Asp Lys Asp Val Phe His Met Val Val
65 35 40 45
66 Glu Val Pro Arg Trp Ser Asn Ala Lys Met Glu Ile Ala Thr Lys Asp
67 50 55 60
68 Pro Leu Asn Pro Ile Lys Gln Asp Val Lys Lys Gly Lys Leu Arg Tyr
69 65 70 75 80
70 Val Ala Asn Leu Phe Pro Tyr Lys Gly Tyr Ile Trp Asn Tyr Gly Ala
71 85 90 95
72 Ile Pro Gln Thr Trp Glu Asp Pro Gly His Asn Asp Lys His Thr Gly
73 100 105 110
74 Cys Cys Gly Asp Asn Asp Pro Ile Asp Val Cys Glu Ile Gly Ser Lys
75 115 120 125
76 Val Cys Ala Arg Gly Glu Ile Ile Gly Val Lys Val Leu Gly Ile Leu
77 130 135 140
78 Ala Met Ile Asp Glu Gly Glu Thr Asp Trp Lys Val Ile Ala Ile Asn
79 145 150 155 160
80 Val Asp Asp Pro Asp Ala Ala Asn Tyr Asn Asp Ile Asn Asp Val Lys
81 165 170 175
82 Arg Leu Lys Pro Gly Tyr Leu Glu Ala Thr Val Asp Trp Phe Arg Arg
83 180 185 190
84 Tyr Lys Val Pro Asp Gly Lys Pro Glu Asn Glu Phe Ala Phe Asn Ala
85 195 200 205
86 Glu Phe Lys Asp Lys Asp Phe Ala Ile Asp Ile Ile Lys Ser Thr His
87 210 215 220
88 Asp His Trp Lys Ala Leu Val Thr Lys Lys Thr Asn Gly Lys Gly Ile
89 225 230 235 240
90 Ser Cys Met Asn Thr Thr Leu Ser Glu Ser Pro Phe Lys Cys Asp Pro
91 245 250 255
92 Asp Ala Ala Arg Ala Ile Val Asp Ala Leu Pro Pro Pro Cys Glu Ser
93 260 265 270
94 Ala Cys Thr Val Pro Thr Asp Val Asp Lys Trp Phe His His Gln Lys
95 275 280 285
96 Asn
97
98
99 (2) INFORMATION FOR SEQ ID NO:2:

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100

101

(i) SEQUENCE CHARACTERISTICS:

102

(A) LENGTH: 1275 base pairs

103

(B) TYPE: nucleic acid

104

(C) STRANDEDNESS: single

105

(D) TOPOLOGY: linear

106

107

(ii) MOLECULE TYPE: cDNA

108

109

(vii) IMMEDIATE SOURCE:

110

(A) LIBRARY:

111

(B) CLONE: Consensus

112

113

(xi) SEQUENCE DESCRIPTION: SEQ ID-NO:2:

114

115

CAAGAGGTTN GGGGCTCTCT CCTTGTCAGT CGGCGCCGCG TGC GGGCTGG TGGCTCTGTG 60

116

GCAGCGGCGG CGGCAGGACT CCGGCACTAT GAGCGGCTTC AGCACCAGAG AGCGCGCCGC 120

117

GCCCTTCTCC CTGGAGTACC GAGTCTTCCT CAAAAATGAG AAAGGACAAT ATATATCTCC 180

118

ATTTTCATGAT ATTCCAATTT ATGCAGATAA GGATGTGTTT CACATGGTAG TTGAAGTACC 240

119

ACGCTGGTCT AATGCAAAAA TGGAGATTGC TACAAAGGAC CCTTTAAACC CTATTAAACA 300

120

AGATGTGAAA AAAGGAAAAC TTCGCTATGT TGCGAATTTG TTCCCGTATA AAGGATATAT 360

121

CTGGAACATAT GGTGCCATCC CTCAGACTTG GGAAGACCCA GGGCACAATG ATAAACATAC 420

122

TGGCTGTTGT GGTGACAATG ACCCAATTGA TGTGTGTGAA ATTGGAAGCA AGGTATGTGC 480

123

AAGAGGTGAA ATAATTGGCG TGAAAGTTCT AGGCATATTG GCTATGATTG ACGAAGGGGA 540

124

AACCGACTGG AAAGTCATTG CCATTAATGT GGATGATCCT GATGCAGCCA ATTATAATGA 600

125

TATCAATGAT GTCAAACGGC TGAAACCTGG CTACTTAGAA GCTACTGTGG ACTGGTTTATG 660

126

AAGGTATAAG GTTCCTGATG GAAAACCAGA AAATGAGTTT GCGTTTAATG CAGAATTTAA 720

127

AGATAAGGAC TTTGCCATTG ATATTATTAA AAGCACTCAT GACCATTGGA AAGCATTAGT 780

128

GACTAAGAAA ACGAATGGAA AAGGAATCAG TTGCATGAAT ACAACTTTGT CTGAGAGCCC 840

129

CTTCAAGTGT GATCCTGATG CTGCCAGAGC CATTGTGGAT GCTTTACCAC CACCCTGTGA 900

130

ATCTGCCTGC ACAGTACCAA CAGACGTGGA TAAGTGGTTC CATCACCAGA AAAACTAATG 960

131

AGATTTCTCT GGAATACAAG CTGATATTGC TACATCGTGT TCATCTGGAT GTATTAGAAG 1020

132

TAAAAGTAGT AGCTTTTCAA AGCTTTAAAT TTGTAGAACT CATCTAACTA AAGTAAATTC 1080

133

TGCTGTGACT AATCCAATAT ACTCAGAATG TTATCCATCT AAAGCATTTT TCATATCTCA 1140

134

ACTAAGATAA CTTTTAGCAC ATGCTTAAAT ATCAAAGCAG TTGTCATTTG GAAGTCACTT 1200

135

GTGAATAGAT GTGCAAGGGG AGCACATATT GGATGTATAT GTTACCATAT GTTAGGAAAT 1260

136

AAAATTATTT TGCTG 1275

137

138

(2) INFORMATION FOR SEQ ID NO:3:

139

140

(i) SEQUENCE CHARACTERISTICS:

141

(A) LENGTH: 114 amino acids

142

(B) TYPE: amino acid

143

(C) STRANDEDNESS: single

144

(D) TOPOLOGY: linear

145

146

(ii) MOLECULE TYPE: peptide

147

148

(vii) IMMEDIATE SOURCE:

149

(A) LIBRARY: GenBank

150

(B) CLONE: 727225

151

152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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153
154 Asn Ile Phe Pro Tyr Lys Gly Tyr Ile Trp Asn Tyr Gly Thr Leu Pro
155 1 5 10 15
156 Gln Thr Trp Glu Asp Pro His Glu Lys Asp Lys Ser Thr Asn Cys Phe
157 20 25 30
158 Gly Asp Asn Asp Pro Ile Asp Val Cys Glu Ile Gly Ser Lys Ile Leu
159 35 40 45
160 Ser Cys Gly Glu Val Ile His Val Lys Ile Leu Gly Ile Leu Ala Leu
161 50 55 60
162 Ile Asp Glu Gly Glu Thr Asp Trp Lys Leu Ile Ala Ile Asn Ala Asn
163 65 70 75 80
164 Asp Pro Glu Ala Ser Lys Phe His Asp Ile Asp Asp Val Lys Lys Phe
165 85 90 95
166 Lys Pro Gly Tyr Leu Glu Ala Thr Leu Asn Trp Phe Arg Leu Tyr Lys
167 100 105 110
168 Val Pro
169
170

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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 585322

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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187 Met Ser Ser Phe Ser Ser Glu Glu Arg Ala Ala Pro Phe Thr Leu Glu
188 1 5 10 15
189 Tyr Arg Val Phe Leu Lys Asn Glu Lys Gly Gln Tyr Ile Ser Pro Phe
190 20 25 30
191 His Asp Ile Pro Ile Tyr Ala Asp Lys Glu Val Phe His Met Val Val
192 35 40 45
193 Glu Val Pro Arg Trp Ser Asn Ala Lys Met Glu Ile Ala Thr Lys Asp
194 50 55 60
195 Pro Leu Asn Pro Ile Lys Gln Asp Val Lys Lys Gly Lys Leu Arg Tyr
196 65 70 75 80
197 Val Ala Asn Leu Phe Pro Tyr Lys Gly Tyr Ile Trp Asn Tyr Gly Ala
198 85 90 95
199 Ile Pro Gln Thr Trp Glu Asp Pro Gly His Asn Asp Lys His Thr Gly
200 100 105 110
201 Cys Cys Gly Asp Asn Asp Pro Ile Asp Val Cys Glu Ile Gly Ser Lys
202 115 120 125
203 Val Cys Ala Arg Gly Glu Ile Ile Arg Val Lys Val Leu Gly Ile Leu
204 130 135 140
205 Ala Met Ile Asp Glu Gly Glu Thr Asp Trp Lys Val Ile Ala Ile Asn

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206      145      150      155      160
207 Val Glu Asp Pro Asp Ala Ala Asn Tyr Asn Asp Ile Asn Asp Val Lys
208      165      170      175
209 Arg Leu Lys Pro Gly Tyr Leu Glu Ala Thr Val Asp Trp Phe Arg Arg
210      180      185      190
211 Tyr Lys Val Pro Asp Gly Lys Pro Glu Asn Glu Phe Ala Phe Asn Ala
212      195      200      205
213 Glu Phe Lys Asp Lys Asn Phe Ala Ile Asp Ile Ile Glu Ser Thr His
214      210      215      220
215 Asp Tyr Trp Arg Ala Leu Val Thr Lys Lys Thr Asp Gly Lys Gly Ile
216      225      230      235      240
217 Ser Cys Met Asn Thr Thr Val Ser Glu Ser Pro Phe Gln Cys Asp Pro
218      245      250      255
219 Asp Ala Ala Lys Ala Ile Val Asp Ala Leu Pro Pro Pro Cys Glu Ser
220      260      265      270
221 Ala Cys Thr Ile Pro Thr Asp Val Asp Lys Trp Phe His His Gln Lys
222      275      280      285
223 Asn
224
225

```

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 4199

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```

241 Met Thr Tyr Thr Thr Arg Gln Ile Gly Ala Lys Asn Thr Leu Glu Tyr
242 1 5 10 15
243 Lys Val Tyr Ile Glu Lys Asp Gly Lys Pro Val Ser Ala Phe His Asp
244 20 25 30
245 Ile Pro Leu Tyr Ala Asp Lys Glu Asn Asn Ile Phe Asn Met Val Val
246 35 40 45
247 Glu Ile Pro Arg Trp Thr Asn Ala Lys Leu Glu Ile Thr Lys Glu Glu
248 50 55 60
249 Thr Leu Asn Pro Ile Ile Gln Asp Thr Lys Lys Gly Lys Leu Arg Phe
250 65 70 75 80
251 Val Arg Asn Cys Phe Pro His His Gly Tyr Ile His Asn Tyr Gly Ala
252 85 90 95
253 Phe Pro Gln Thr Trp Glu Asp Pro Asn Val Ser His Pro Glu Thr Lys
254 100 105 110
255 Ala Val Gly Asp Asn Asp Pro Ile Asp Val Leu Glu Ile Gly Glu Thr
256 115 120 125
257 Ile Ala Tyr Thr Gly Gln Val Lys Gln Val Lys Ala Leu Gly Ile Met
258 130 135 140

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SEQUENCE CORRECTION REPORT
PATENT APPLICATION US/09/415,540

DATE: 11/09/1999
TIME: 15:46:27

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Line	Original Text	Corrected Text
3	(1) General Information	(1) GENERAL INFORMATION:
8	(ii) TITLE OF THE INVENTION: A NOVEL HUMAN PY	(ii) TITLE OF INVENTION: A NOVEL HUMAN PYROP